

Figure S1. Coverage of the rabies genome.

A schematic representation of the RABV genome is shown at the top of the figure. The average number of mapped reads are per position projected along the RABV genomic position. Peaks are related to PCR fragments overlapping areas. (A) *In vitro* experiments. (B) *In vivo* experiments. The different colors correspond to different samples (different passages in animals or in cells)

